

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2002, 00:12:12 ; Search time 1693.08 Seconds

(without alignments)
11838.176 Million cell updates/sec

Title: US-09-088-435-2

Perfect score: 1485

Sequence: 1 GGGTCGACACCGTCGCATG.....TTCTGATTCGAAAAAAA 1485

Scoring table:

IDENTITY_NUC
Gapop 10.0, Gapept 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	773	52.1	773	10	BG679339
2	748	50.4	845	10	B1858271
3	744.2	50.1	815	10	BG702609
4	736.4	49.6	948	10	BG749122
5	726.4	48.9	807	10	BG473546
6	712.2	48.0	1099	10	BM463961
7	677	45.6	732	10	BF056112
8	666	44.8	667	10	BG774012
9	663.4	44.7	716	10	BG912245
10	646	43.5	679	9	A1953998
11	638	43.0	666	9	A1741818
12	605	40.7	606	9	BE222929
13	603	40.6	645	10	BE273896
14	587.2	39.5	964	10	BG169868
15	583.6	39.3	614	9	AA573827
16	563	37.9	700	10	B1670014
17	561.6	37.8	577	9	A1742027

18	517.8	34.9	570	10	BM129226
19	506.6	34.1	574	10	BM129278
20	502.6	33.8	807	10	BE768991
21	498.2	33.5	856	10	BE785282
22	492.2	33.1	806	10	BG968751
23	482.4	32.5	897	10	BG437057
24	480	32.3	480	10	BF064129
25	459.6	30.9	824	11	AK014487
26	449.4	30.3	451	9	A1344703
27	447.4	30.1	450	9	A1687918
28	435.2	29.3	600	10	BF780159
29	431.2	29.0	436	9	AM613258
30	427.2	28.8	591	10	B1359570
31	425.6	28.7	560	9	AM654331
32	425	28.6	602	9	BE134859
33	423.6	28.5	559	9	AM654338
34	417	28.1	418	9	A1241423
35	406.8	27.4	501	10	BE619177
36	400.8	27.0	573	10	B1682987
37	394.6	26.6	555	9	AM658374
38	394	26.5	546	9	AM656343
39	392	26.4	551	9	AM654557
40	392	26.4	565	10	B1541815
41	387.6	26.1	545	9	AM655435
42	386	26.0	562	9	AM656964
43	384.6	25.9	700	10	BE963955
44	378	25.5	542	9	AM656338
45	369.6	24.9	448	10	BF064050

ALIGNMENTS

RESULT 1
LOCUS BG679339 773 bp mRNA linear EST 01-MAY-2001
DEFINITION 602628516F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4753394 5',
LOCUS BG679339.1 GI:19910723
VERSION BG679339.1
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 773)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strusberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: James Cleaver, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM10612 row: P column: 03
High quality sequence starters 772.
Location/Qualifiers
1. 773
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4753394"
/clone_lib="NCI_CGAP_Skn4"
/tissue_type="squamous cell carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: skin; Vector: pCMV-Sport6; Site_1: NCI;
Site_2: Salt; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5kb. Library constructed by Life
Technologies. Note: this is a NCI_CGAP Library."

BASE COUNT

142 a 208 c 279 g 144 t

Authors	Title	Journal	Comment
NIH-MGC	http://mgc.ncl.nih.gov/	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabds-remail.nih.gov

NIH-MGC <http://mgc.ncl.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC),
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: DCTD/DPH
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLT at:
<http://image.lnlt.gov>
Plate: LHAM2001 row: e column: 10
High quality sequence stop: 819

Location/Qualifiers
1 845

/cd_xref="tomo sapiens"
 /clone IMAGE:5392881"
 /clone_id="NH_MGC-87"
 /tissue_type="mammary adenocarcinoma, cell line"
 /note="p53-DH10 (phage-resistant)"
 Site:2: Organ: breast; Vector: pCMV-Sport6; Site:1: NotI
 Average insert size 1.383 kb. Library enriched for
 full-length clones and constructed by Life Technologies.
 Note: This is a NIH MGC Library.

643. AGGTCCTGGACGAGGCCAATCTGAGGGCCCAATTGTTTGT
.....
.....

indels. 4; Gaps 4;

QY	643	AGGCTCTGGGACGAGGCCAATCTGAGGGCGCAAGAGTTGGCCAMAGAGGAGCGCTGGAGA	700
Dd	40	AGGCTCTGGGACGAGGCCAATCTGAGGGCGCAAGAGTTGGCCAMAGAGGAGCGCTGGAGA <td>700</td>	700
QY	703	ATGTCCCCCGTTTGACCAACCCCCCTAAATATGAAAGGCCACGCGACGCTGTGTGCAGAGAC <td>99</td>	99
Dd	100	ATGTCCCCCGTTTGACCAACCCCCCTAAATATGAAAGGCCACGCGACGCTGTGTGCAGAGAC <td>76</td>	76
QY	763	TGAAGAAGCATGTGTAGGACCCCCACACAGTGCCCTGTGTGTGCAGTGTGGGTGGGGGTC <td>15</td>	15
Dd	160	TGAAGAAGCATGTGTAGGACCCCCACACAGTGCCCTGTGTGTGCAGTGTGGGTGGGGGTC <td>82</td>	82
QY	823	TGCTGGCGGGGGTGTGTGTGTGGCCCTCTGAGAGTGGGCTGCGAGCATATGCCATCATTTG <td>219</td>	219
Dd	220	TGCTGGCGGGGGTGTGTGTGTGGCCCTCTGAGAGTGGGCTGCGAGCATATGCCATCATTTG <td>882</td>	882
QY	883	CCATGAGACCCCATGGGGGACACACTGTTCAA-TGCGGCCATCACAGCGGGCAGAGTGTC <td>279</td>	279
Dd	280	CCATGAGACCCCATGGGGGACACACTGTTCAA-TGCGGCCATCACAGCGGGCAGAGTGTC <td>941</td>	941
QY	942	ACACTTTCAGCAATCACCAAGCTGTGGCCAAAGAGCCTGGGTGCTCAAGAGCCTGGGGGTC <td>339</td>	339

Accession	Sequence	Position
Db	340 ACACTTCAGACATCACCAATGTGGCCAAAGACCTGGGTGCAGAGAGTGTCGCTCG	10
Qy	1002 GCCCTGGAGTGCATGCAGGTGTCAAGATTCCTTGAAGTGTGGAGACACCGAGCT	39
Db	400 GCCCTGGAGTGCATGCAGGTGTGCAAGATTCCTTGAAGTGTGGAGACACCGAGCT	10
Qy	1062 GTGAGCCTTGCAGCAGCTCCTGGATATAGAGTATGCTGGTGGAGCTCCCTGTGGG	112
Db	460 GTGAGCCTTGCAGCAGCTCCTGGATATAGAGTATGCTGGTGGAGCTCCCTGTGGG	112
Qy	1122 GCAGCCTTGCAGCAGCATCTACTCAGGCTCCTGCGAGAGCTCCAGCGCAGAGGCTGCTG	519
Db	520 GCAGCCTTGCAGCAGCATCTACTCAGGCTCCTGCGAGAGCTCCAGCGCAGAGGCTGCTG	118

Db 580 CCCCCTCCCTGACTGCTGATCTGCTGTGTGGAGGCAACATCAACAGCCGA 639

OY 1242 GAGGTGAGGCTTTGAAACACCACTGGGCGAGGCTGAGGGGTCCCTCTGG-CCCCA 1300
|||||

Db 640 GAGTGCAGGCTTTGAAACACCACTGGGCGAGGCTGAGGGGTCCCTCTGG-CCCCA 699
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OY 1301 AAGACCCCTGAGAGGCCCATGAGACGTCCTGTCTGTGATGAGAGGAGCATGCTGGC 1360
|||||

Db 700 AAGACCCCTGAGAGGCCCATGAGACGTCCTGTCTGTGATGAGAGGAGCATGCTGGC 759
|||||

OY 1361 AGATGGCAGTGG-AGAGTGGCCTGTGCACTGTGCTGCTCTCTTAAGAGGCCCTC 1419
|||||

Db 760 AGATGGCAGTGGAGAGGCTGGCCCTGTGCAATGTGCTGCTCTCTTAAGAGGCCCTC 819
|||||

OY 1420 C-TGAGCTGCTCTTTGGCTCTC 1442
|||||

Db 820 CTGGAGCTGCTCTTTGGCTCTC 843
|||||

RESULT 3
BG702609 815 bp mRNA linear EST 07-MAY-2001
LOCUS 602684322F1 NIH_MGC_95 Homo sapiens cDNA clone IMAGE:4817021.5,
DEFINITION mRNA sequence.
ACCESSION BG702609
VERSION BG702609.1 GI:13974113
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 815)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@fslmail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiroki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
plate: LMA10716 row: k column: 06
High quality sequence stop: 811.
Location/Qualifiers
1. 815
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4817021"
/clone_id="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
/note="Organ: brain; Vector: pBluescript (modified
pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTVN-3',
size-selected for average insert size 2.5 kb and
normalized to R0.5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIH/NHGRI, National
Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 149 a 216 c 300 g 149 t 1 others

ORIGIN

Query Match 50.1%; Score 744.2; DB 10; Length 815;
Best Local Similarity 98.2%; Pred. No. 1.7e-158;
Matches 805; Conservative 0; Mismatches 9; Indels 6; Gaps 5;

OY 201 AGCTGTTCCCTGGCAGGCTGAGGCGCAGAGCTGGGCGCAGCTGCTGTGATAGTTG 260

Db 1 AGCGGTTCCCTGGCAGGCTGAGGCGCAGAGCTGGGCGCAGCTGTGATAGTTG 60
|||||

OY 261 GCGAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAG 320
|||||

Db 61 GCGAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAG 120
|||||

OY 321 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAG 380
|||||

Db 121 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAG 180
|||||

OY 381 GCGATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 440
|||||

Db 181 GCGATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 240
|||||

OY 441 GCGATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 500
|||||

Db 241 GCGATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 300
|||||

OY 501 TCAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 560
|||||

Db 301 TCAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 360
|||||

OY 561 ACCATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 620
|||||

Db 361 ACCATGCTGTCTTCAGATGAGAGGCTGTGGCAGAGATGCCAAGATTCGCG 420
|||||

OY 621 GCGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 680
|||||

Db 421 GCGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 480
|||||

OY 681 GCGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 740
|||||

Db 481 GCGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 539
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OY 741 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 800
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Db 540 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 599
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OY 801 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 860
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Db 600 CAGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 659
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OY 861 TGGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 920
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Db 660 TGGGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 716
|||||

OY 921 ATCAGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 980
|||||

Db 717 ATCAGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 775
|||||

OY 981 GCGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 1020
|||||

Db 776 G-CAGAGGCTGTGTACCTGTCTTCAGATGAGAGGCTGTGGCAGAGATTCGCG 814
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RESULT 4
BG749122 948 bp mRNA linear EST 15-MAY-2001
LOCUS 602706734F1 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:4843329.5,
DEFINITION mRNA sequence.
ACCESSION BG749122
VERSION BG749122.1 GI:14059775
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 948)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LCM1679 row: c column: 10
 High quality sequence stop: 802.

FEATURES

source
 1. 948
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4843329"
 /clone.lib="NIH_MGC_43"
 /tissue.type="normal pigmented retinal epithelium"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site: 1; XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 185 a 238 c 345 g 180 t
 ORIGIN

Query Match 49.6%; Score 736.4; DB 10; Length 948;
 Best Local Similarity 93.08; Pred. No. 1e-156;
 Matches 859; Conservative 0; Mismatches 56; Indels 9; Gaps 8;

QY 228 AGGAGCTGGGGCCACGCTGGTGGGATGTTGGGAGGAGGCGTGTCTACCTGGTTC
 Db 2 AGGAGCTGGGGCCACGCTGGTGGGATGTTGGGAGGAGGCGTGTCTACCTGGTTC 61
 QY 288 AGAATGAGACGGCCCTGTGGGAGAGATGCCAGACAGAGCCCTTTCACGTGACACT 347
 Db 62 AGAATGAGACGGCCCTGTGGGAGAGATGCCAGACAGAGCCCTTTCACGTGACACT 121
 QY 348 CTGTGGAGAGCTGGGCGTGTCCAGAGTGGCGGATGCTGTCTCTCAAGTGTGAG 407
 Db 122 CTGTGGAGAGCTGGGCGTGTCCAGAGTGGCGGATGCTGTCTCTCAAGTGTGAG 181
 QY 408 AATGTGAGCCGAGCGGCTCTCAAGATTCGGGCAATTCGATTTCCAGAGAGATG 467
 Db 182 AATGTGAGCCGAGCGGCTCTCAAGATTCGGGCAATTCGATTTCCAGAGAGATG 241
 QY 468 GCCAAGAGAGATGACAGACCTGTGTCTCTCAAGGGGTAATGCGGGATTCCTGT 527
 Db 242 GCCAAGAGAGATGACAGACCTGTGTCTCTCAAGGGGTAATGCGGGATTCCTGT 301
 QY 528 GCGTATGCTGAGAGAGTGGGCAATTCGTCACCATGCTCTCCGAGAGACCTCC 587
 Db 302 GCGTATGCTGAGAGAGTGGGCAATTCGTCACCATGCTCTCCGAGAGACCTCC 361
 QY 588 CTGACAGTGTGTCAGAGGCTGTCAGGGGAGGGGCGGAGTTCACTACGTGAAAGTGC 647
 Db 362 CTGACAGTGTGTCAGAGGCTGTCAGGGGAGGGGCGGAGTTCACTACGTGAAAGTGC 421
 QY 648 TGGGAGAGAGCAATCTGAGGGCGCAAGAGTTGGCCAAAGAGGAGGCTGGAGATGTC 707
 Db 422 TGGGAGAGAGCAATCTGAGGGCGCAAGAGTTGGCCAAAGAGGAGGCTGGAGATGTC 481
 QY 708 CCCCCGTTTGACACCCCTATATGAAAGCCACGACCTGTGTGACAGAGCTGAAA 767
 Db 482 CCCCCGTTTGACACCCCTATATGAAAGCCACGACCTGTGTGACAGAGCTGAAA 541
 QY 768 GCAGTGTGAGAGCCCAACAGAGTGGCTGTGTGAGTTGGGGGGGCTCTCTG 827
 Db 542 GCAGTGTGAGAGCCCAACAGAGTGGCTGTGTGAGTTGGGGGGGCTCTCTG 601

QY 828 GCCGGGTGTGTGC-TGGCTGTGAGAGTGGGTGGCAGCATGTACCATTTGCCAT 886
 Db 602 AGCGGGGTGGGTGCTGTGGCTGTGAGAGTGGGTGGCAGCATGTACCATTTGCCAT 639
 QY 887 GGAGACCATGGGGCACACCTGCTTCATGCGGCCATACACCGGCAAGTGTGCACACT 946
 Db 660 TGGAGACCATGGGGCACACCTGCTTCATGCGG-CATACAG-CGGCAAGCTGTGCACACT 717
 QY 947 TCCAGACTTACCAAGTGTGGCCAAAGAGCTGGGTGTCACAAAGAGTGGCGCCCT 1006
 Db 718 TCCAGACTTACCAAGTGTGGCCAAAGAGCTGGGTGTCACAAAGTGGCGCCCT 775
 QY 1007 GGAATGATGAGAGTGTGCAAGATTCATCTGAG-TGGTGGAGACACCGAGCTGTGA 1065
 Db 776 GAGTGTGATGAGAGTGTGCAAGATTCATCTGAAAGTGTGGAGGACACCGAGCTGTG 835
 QY 1066 GCGGTGTGACAGACTTCCTGATGATGAGCGTATGCTGTGGAGAGCTGTGGGCGAG 1125
 Db 836 AACGCTGTGACAGAGCTGTGATGAAAGGATTAACGAGTGAACCTCTGTGGGACA 895
 QY 1126 CTTAGACGACCATCTCAAGGCC 1149
 Db 896 CTTAG-TAGCATTTAATCAAGGCC 918

RESULT 5
 LOCUS BG473546 807 bp mRNA linear EST 21-MAR-2001
 DEFINITION 602516083f1 NIH_MGC_16 Homo sapiens cDNA clone IMAGE:4647572.5
 ACCESSION BG473546
 VERSION BG473546.1 GI:13405821
 KEYWORDS EST
 SOURCE human
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 807)
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-r@mail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
 Plate: LCM1424 row: f column: 21
 High quality sequence stop: 802.

FEATURES

source
 1. 807
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4647572"
 /clone.lib="NIH_MGC_16"
 /tissue.type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pOTB7; Site: 1; XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Library constructed by Ling Hong
 in the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."
 BASE COUNT 148 a 220 c 291 g 148 t
 ORIGIN

Query Match

48.9%; Score 726.4; DB 10; Length 807;

QY 803 GGCAGTTGGGGGTGGGGG-----TCTCTGCGCGGGGTGGTGGCTGG-CCTCTGGAGATG 857
 Db 609 GGATTGGGGGGGGGGGGGGTCTCCCTGCGCGGGGGTGGTGGCTGGCTGGCTGGAGT 857
 QY 858 GCGCGGAGCATGTACCCATCATTTGCAATGAGACCCATGGGGACACCTGCTTCAATGCG 858
 Db 669 GGGTGGCCCTGTTTCTCCCTCTTGGCTGGACCCCTGGGGCCCTTGGCTTCTCCG 858
 QY 918 GGCATCAGACCGGACGCTGGTGCACACTTCCAGACATCAGACATGAGGACAGATTC 917
 Db 729 GCGCTCCCGGGCGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGG 917
 QY 978 GGTCCAGAGAGGTGGCGCCG-TGGGGCCCTGGAGTGCATGAGTGGTGGCAATTCAC 977
 Db 789 GTTGGCCAGACGTGGCGCCCTTGGCGCCCTGGAGTGGCTGGCTGGCTGGCTGGCTGG 977
 RESULT 7 732 bp mRNA linear EST 16-OCT-2000
 LOCUS BF056112.1
 DEFINITION 732 bp mRNA linear EST 16-OCT-2000
 7387805.x1 Soares NSF_F8_9W_OT_P1.P.S1 Homo sapiens cDNA clone
 IMAGE:339393 3' similar to SW:SDHL.RAT P09367 L.SERINE
 DEHYDRATASE/L-THEONINE DEAMINASE [INCLUDES: L-SERINE DEHYDRATASE
 mRNA sequence.
 BF056112.1 GI:10810008
 EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC1-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP).
 Tumor Gene Index
 Unpublished (1997)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 This clone is available royalty-free through LLMN; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Seq primer: -400p from Gluco
 High quality sequence stop: 417.
 FEATURES
 source
 1. 732
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:339393"
 /lab_host="DH10B"
 /note="Organ: pooled; Vector: p773D-Pac (Pharmacia) with
 a modified polylinker; Site: 1: Not I; Site 2: Eco RI;
 Equal amounts of plasmid DNA from five normalized
 libraries were mixed, and ss circles were made in vitro.
 Following HAP purification, this DNA was used as tracer in
 a subtractive hybridization reaction. The driver was
 the same 5 libraries. The pools consisted of the following
 libraries and clones: Soares NBHF pool 1:
 309384-310919, 323208-325895 Soares NBHF pool 1:
 145032-147335, 147720-148103, 148872-149255, 15002
 150407, 151176-152327 Soares NBHF pool 1:
 758280-760583, 772104-774407 Soares NBHF pool 1:
 304776-306311, 320136-322823, 326280-326653 Soares NBHF
 pool 1: 723720-726407, 739080-740999 Subtraction by Bento
 Soares and M. Fatima Bonaldo."
 BASE COUNT 150 a 223 c 195 g 164 t
 ORIGIN

Query Match 45.6%; Score 677; DB: 10; Length 732;
 Best Local Similarity 97.2%; Pred. No. 2.9e-143;
 Matches 689; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 777 AGGACCCACAGAGTGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 836
 Db 732 AGTACCCACAGAGTGGCCCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 836
 QY 837 GTGGCGGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 837
 Db 672 GTGGCGGCGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 837
 QY 897 GGGGACACTGCTTCAATGCGGCGGCTGCACACCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 Db 612 GGGGACACTGCTTCAATGCGGCGGCTGCACACCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 QY 957 ACCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 Db 552 ACCAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 QY 1017 CAGGTGTCAAGATTCACTCTGAAGTGGTGGAGAGACAGGAGGCTGTGGAGGCTGTGGAG 837
 Db 492 CAGGTGTCAAGATTCACTCTGAAGTGGTGGAGAGACAGGAGGCTGTGGAGGCTGTGGAG 837
 QY 1077 CAGGTGTCAAGATTCACTCTGAAGTGGTGGAGAGACAGGAGGCTGTGGAGGCTGTGGAG 837
 Db 432 CAGGTGTCAAGATTCACTCTGAAGTGGTGGAGAGACAGGAGGCTGTGGAGGCTGTGGAG 837
 QY 1137 ATCTACACAGGCTCTGTGGAGGCTGTGGAGGCTGTGGAGGCTGTGGAGGCTGTGGAG 837
 Db 372 ATCTACACAGGCTCTGTGGAGGCTGTGGAGGCTGTGGAGGCTGTGGAGGCTGTGGAG 837
 QY 1197 TCAGTGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837
 Db 312 TCAGTGTGGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 837
 QY 1257 AAACCCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 Db 253 AAACCCACAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 837
 QY 1317 CCATGACAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
 Db 192 CCATGACAGTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 837
 QY 1377 TGCCCTGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 837
 Db 132 TGCCCTGTCAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 837
 QY 1437 GCTTCCGACAACTCGGCGCAATTAACACTTCTGAAATTAACAAATTAACAAATTAACAA 837
 Db 72 GCTTCCGACAACTCGGCGCAATTAACACTTCTGAAATTAACAAATTAACAAATTAACAA 837
 RESULT 8
 LOCUS BG774012 667 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602661747F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4810186 5'
 mRNA sequence.
 BG774012
 ACCESSION BG774012.1 GI:1404311
 VERSION BG774012.1
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://nigc.ncbi.nlm.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 CONTACT: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Ling Hong/Rubin Laboratory
 DNA sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10M1665 row: n column: 11
 High quality sequence stop: 667.

FEATURES

Source

Location/Qualifiers
 1. 667

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4810186"
 /clone_lib="NIH.MGC.21"
 /tissue_type="choriocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: placenta; Vector: pOTB7; site_1: XhoI;
 site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCAGCAG(C). Size selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the Laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."
 BASE COUNT 116 a 176 c 251 g 124 t
 ORIGIN

Query Match 44.8%; Score 666; DB 10; Length 667;
 Best Local Similarity 100.0%; Pred. No. 8,7e-141;
 Matches 666; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

209 CCCTGGCAGGCTGGAGGCGAGAGCTGGGGCCAGCTGCTGGGATGATTGGCAGGGA 268
 |||||||
 2 CCCTGGCAGGCTGGAGGCGAGAGCTGGGGCCAGCTGCTGGGATGATTGGGAGGGA 61
 |||||||
 269 GGCCTGTACCTGCTGCTCAGCAATGAGAGCGCCCTGTGGCAGAGCATGCCAGAGAGCC 328
 |||||||
 62 GGGTGTACCTGCTGCTCAGCAATGAGAGCGCCCTGTGGCAGAGCATGCCAGAGAGCC 121
 |||||||
 339 CTTTACGCTGTGACACCTCTGTGGAAGAGCTGGCGCTGTCCAGAGTGGCGGATGCC 388
 |||||||
 122 CTTTACGCTGTGACACCTCTGTGGAAGAGCTGGCGCTGTCCAGAGTGGCGGATGCC 181
 |||||||
 389 TGTCTCTCAAGTGTGAAGATGTCAGCCCGGCTCTTCAAGATTGGGGCATGG 448
 |||||||
 182 TGTCTCTCAAGTGTGAAGATGTCAGCCCGGCTCTTCAAGATTGGGGCATGG 241
 |||||||
 449 GCATTTCGCAAGAGATGAGCAAGAGGATGACAGACCTGTGTGCTCTCAGGGGG 508
 |||||||
 242 GCATTTCGCAAGAGATGAGCAAGAGGATGACAGACCTGTGTGCTCTCAGGGGG 301
 |||||||
 509 TAATGCGGGCATGCTGCTGCTATGCTGTAGAAAGCTGGGCAATTCCTGCCACCATGCT 568
 |||||||
 302 TAATGCGGGCATGCTGCTGCTATGCTGTAGAAAGCTGGGCAATTCCTGCCACCATGCT 361
 |||||||
 569 GCTCCCGAGAGACCTCTCTGCAAGTGTGAGAGCTGCAAGGGGAGAGGGCCGAGGT 628
 |||||||
 362 GCTCCCGAGAGACCTCTCTGCAAGTGTGAGAGCTGCAAGGGGAGAGGGCCGAGGT 421
 |||||||
 629 TCAGTGAAGTGAAGAGTGTGGAGAGAGCCCAATCTGAGGGGCAAGAGTTGGCAAGAG 688
 |||||||
 422 TCAGTGAAGTGAAGAGTGTGGAGAGAGCCCAATCTGAGGGGCAAGAGTTGGCAAGAG 481
 |||||||
 689 GAGCGGCTGGAGAGATGTCCTCCGTTTGACACCCCTTAATATGAGAAAGGCCAGCCAG 748
 |||||||
 482 GAGCGGCTGGAGAGATGTCCTCCGTTTGACACCCCTTAATATGAGAAAGGCCAGCCAG 541
 |||||||
 749 CCTGTGAGAGAGTGAAGAGTGTGAGAGAGCCCAAGTGTGGCTGTGCTGTGGCAAT 808
 |||||||
 542 CCTGTGAGAGAGTGAAGAGTGTGAGAGAGCCCAAGTGTGGCTGTGCTGTGGCAAT 601
 |||||||
 809 TGGGGGTGGGGTCTCTGAGCGGGGGTGGTGGCTGGCTGTGAGAGTGGCTGGCAGCA 868
 |||||||
 602 TGGGGGTGGGGTCTCTGAGCGGGGGTGGTGGCTGGCTGTGAGAGTGGCTGGCAGCA 661
 |||||||
 869 TGTACC 874

Db 662 TGTACC 667
 |||||||

RESULT 9

LOCUS

602806987F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939221

DEFINITION

5', mRNA sequence.

ACCESSION

602806987F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939221

VERSION

602806987F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4939221

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 716)
 NIH-MGC http://mgi.nhl.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs.rem@nih.gov
 Tissue Procurement: David N. Louis, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L10M10875 row: n column: 22
 High quality sequence stop: 695.

AUTHORS

NIH-MGC

TITLE

Unpublished (1999)

JOURNAL

Unpublished (1999)

COMMENT

Unpublished (1999)

FEATURES

Source

Location/Qualifiers
 1. 716

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4939221"
 /clone_lib="NCI CGAP_Brn67"
 /tissue_type="anaplastic oligodendroglioma with 1p/19q
 loss"
 /lab_host="DH10B (T1 phage-resistant)"
 /note="Organ: brain; Vector: pCMV-SPORT6; site_1: NotI;
 site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.3 kb. Constructed by Life
 Technologies. Note: this is a NCI CGAP Library."
 BASE COUNT 137 a 208 c 230 g 141 t
 ORIGIN

Query Match 44.7%; Score 663.4; DB 10; Length 716;
 Best Local Similarity 99.4%; Pred. No. 3.5e-140;
 Matches 697; Conservative 0; Mismatches 1; Indels 3; Gaps 3;

780 ACCCCACAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 839
 |||||||
 1 ACCCCACAGGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60
 |||||||
 840 GGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 899
 |||||||
 61 GGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
 |||||||
 900 GCACACTGCTTCAATGCGGCTATCAACAGCGGCAAGCTGTGACACTTCCAGACATCAC 959
 |||||||
 121 GCACACTGCTTCAATGCGGCTATCAACAGCGGCAAGCTGTGACACTTCCAGACATCAC 180
 |||||||
 960 AGTGTGGCCAAAGAGCTGGGTGCAAGAGCGGTGGCGCTGCGGGCCCTGAGATGATGAG 1019
 |||||||
 181 AGTGTGGCCAAAGAGCTGGGTGCAAGAGCGGTGGCGCTGCGGGCCCTGAGATGATGAG 240
 |||||||
 1020 GGTGTGAAGATTCACCTGTAAGTGGTGGAGACACCGAGATGCTGTAGAGCTGTGAGCAG 1079
 |||||||
 241 GTGTGACATTCACCTGTAAGTGGTGGAGACACCGAGATGCTGTAGAGCTGTGAGCAG 300
 |||||||
 1080 CTCCTGATGATGAGCGTATGCTGTGTGAGAGCTGCTGTGTGGGCAAGCTTACAGCAGCATC 1139

Db 301 CTCCGATGATGAGCGATATCTGTGTGAGAGCTTGTGGGCGACCTTAGCAGCCATC 360
 QY 1140 TACTAGAGCCCTCTGCGAGAGCTCCAGGCCGAGGGCTGCTGCCCCCTTCCCTGACTTCA 1199
 Db 361 TACTAGAGCCCTCTGCGAGAGCTCCAGGCCGAGGGCTGCTGCCCCCTTCCCTGACTTCA 419
 QY 1200 GTTGTGTAATCTGTGTGAGAGCAACA-CATCAACGCGGAGAGCTGCGAGCTTTGAA 1258
 Db 420 GTTGTGTAATCTGTGTGAGAGCAACAACACATTAACGCGGAGAGCTGCGAGCTTTGAA 479
 QY 1259 AACCCACTGGGCCAGCTGTGAGGGGTCCTCATCTGCGGCCCAAGACCCCTGAGAGGCC 1318
 Db 480 AACCCACTGGGCCAGCTGTGAGGGGTCCTCATCTGCGGCCCAAGACCCCTGAGAGGCC 539
 QY 1319 ATGACAGCTCTGTGTGTGATGAGAGAGACTAGTGTGCGAGATGCGAGTGAAGCTG 1378
 Db 540 ATGACAGCTCTGTGTGTGATGAGAGAGACTAGTGTGCGAGATGCGAGTGAAGCTG 599
 QY 1379 CCTGTGCAACTGTGTGTGCTGCTCTCTGGAAGAGCCCTGCTGCTGCTTTGGC 1438
 Db 600 -CCTGTGCAACTGTGTGTGCTGCTCTCTGGAAGAGCCCTGCTGCTGCTTTGGC 658
 QY 1439 TCTCCGACAACTCGGCCAATAAACACTTCTGTAATTGAA 1479
 Db 659 TCTCCGACAACTCGGCCAATAAACACTTCTGTAATTGAA 699
 RESULT 10
 A1953998/c 679 bp mRNA linear EST 09-MAR-2000
 LOCUS DEFINITION wx78c12.x1 NCI-CGAP_Ov38 Homo sapiens CDNA clone IMAGE:2549782 3
 sequence. similar to SW:SDHL_RAT P09367 L-SERINE DEHYDRATASE, mRNA
 A1953998.1 GI:5746308
 EST.
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 679)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Jeff Struening, M.D., Michael R. Emmert-Buck,
 M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA
 Library Arrayed by: Christa Prange, The I.M.A.G.E. Consortium DNA
 Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI at:
 www.bio.jhu.edu/bhrp/image/image.html
 Insert length: 2656 Std Error: 0.00
 Seq primer: -400p from G1bco
 High quality sequence stop: 381.
 Location/Qualifiers
 1. 679
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:2549782"
 /clone_lib="NCI-CGAP_Ov38"
 /tissue_type="normal epithelium"
 /lab_host="DH10B"
 /note="Organ: ovary; Vector: pCMV-Sport6; Site: 1; Salt,
 site: 2; NCI: Cloned unidirectionally; Primer: Oligo dT,
 library constructed by Life Technologies."
 BASE COUNT 137 a 215 c 191 g 129 t 7 others
 ORIGIN

Query Match 43.5%; Score 646; DB 9; Length 679;
 Best Local Similarity 97.6%; Pred. No. 3e-136;
 Matches 652; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 809 TGGGGGTGGGGGTCTCTGCGCGGGGGTGTGCTGCTGCTCTGAGAGTGGCGACGA 868
 Db 668 TGGGGGTGGGGGTCTCTGCGCGGGGGTGTGCTGCTGCTCTGAGAGTGGCGACGA 609
 QY 869 TGTACCATCATGTCATGAGAGAGCCCATGAGGAGCACTGTTCAATGGCGCCATCAGC 928
 Db 608 TGTANCCATCATGTCATGAGAGAGCCCATGAGGAGCACTGTTCAATGGCGCCATCAGC 549
 QY 929 CCGCAGCTGTGTACACTTCCAGACATCACCAGTGTGGCCAAAGAGCTTGGCCAAAGC 988
 Db 548 CCGCAGCTGTGTACACTTCCAGACATCACCAGTGTGGCCAAAGAGCTTGGCCAAAGC 489
 QY 989 GGTGGCGGCTGGGGGCTGGAGTGCATGACAGTGTGTGCAATTCACCTGTAAGTGTGA 1048
 Db 488 GGTGGCGGCTGGGGGCTGGAGTGCATGACAGTGTGTGCAATTCACCTGTAAGTGTGA 429
 QY 1049 GGAACCGAGAGCTGTGAGCGCTGTGAGAGAGCTCTGATGATGAGAGCTGTGTA 1108
 Db 428 GGAACCGAGAGCTGTGAGCGCTGTGAGAGAGCTCTGATGATGAGAGCTGTGTA 369
 QY 1109 GCTGCTGTGGGGCAGCCTTACAGACCATCTAAGGCTCTGCGAGAGCTCCAGGC 1168
 Db 368 GCTGCTGTGGGGCAGCCTTACAGACCATCTAAGGCTCTGCGAGAGCTCCAGGC 309
 QY 1169 CGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1228
 Db 308 CGAGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 249
 QY 1229 CATCAACAGCCGAGAGCTGAGGCTTTGAAACCCAGCTGGCCAGAGTGTGGGGTCCC 1288
 Db 248 CATCAACAGCCGAGAGCTGAGGCTTTGAAACCCAGCTGGCCAGAGTGTGGGGTCCC 189
 QY 1289 ATCCTGGCCCAAGAGAGCCCTGAGAGAGCCCATGAGAGCTGTGTGTGATGAGAGAGA 1348
 Db 188 ATCCTGGCCCAAGAGAGCCCTGAGAGAGCCCATGAGAGCTGTGTGTGATGAGAGAGA 129
 QY 1349 CTCAGTGTGCGAGATGAGAGAGTGGAGAGTGGCTGTGCAACTGTGCTGCTGCTGCTGA 1408
 Db 128 CTCAGTGTGCGAGATGAGAGAGTGGAGAGTGGCTGTGCAACTGTGCTGCTGCTGCTGA 69
 QY 1409 AGGAAGCCCTCTGAGAGCTTCTTTGGCTTCCGACAACTCGGCCAATAACACTTT 1468
 Db 68 AGGAAGCCCTCTGAGAGCTTCTTTGGCTTCCGACAACTCGGCCAATAACACTTT 9
 QY 1469 CTGAATTG.1476
 Db 8 CTGAATTG.1
 RESULT 11
 A1741818/c 666 bp mRNA linear EST 19-DEC-1999
 LOCUS DEFINITION wq29c09.x1 Soares NSF_P8_9W_OT_P4_P51 Homo sapiens CDNA clone
 IMAGE:2366512 3' similar to SW:SDHL_RAT P09367 L-SERINE DEHYDRATASE
 mRNA sequence.
 A1741818
 A1741818.1 GI:5110106
 EST.
 VERSION A1741818
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 666)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncigap.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 JOURNAL COMMENT

Query Match	Best Local Similarity	Score	DB	Length
Matches 628; Conservative	98.9%	Pred. No. 1,7e-126	0; Mismatches 5; Indels 2; Gaps 2	
Query 225	GGCAGAGAGCTGGGGCCACAGCTGGTGGGAGTATAGTTGGGAGAGG-AGCGTGTACTTGGT	283		
Db 1	GGCAGAGAGCTGGGGCCACAGCTGGTGGGAGTATAGTTGGGAGAGGAGCGTGTACTTGGT	60		
Query 284	CTCCAGAAATGAGAGCGCCCTGGGAGAGATCCCAAGCAGAGAGCCCTTCACAGTGGTAC	343		
Db 61	CTCCAGAAATGAGAGCGCCCTGGGAGAGATCCCAAGCAGAGAGCCCTTCACAGTGGTAC	120		
Query 344	ACCTCTGTTTGGAGAGCTGGGGCGCTCTCCAGGTGGGGGAGCATGCCCTGTTCTTCACAGT	403		
Db 121	ACCTCTGTTTGGAGAGCTGGGGCGCTCTCCAGGTGGGGGAGCATGCCCTGTTCTTCACAGT	180		
Query 404	TGAGAAATGTCAGAGCCACAGCGGCTCTTCAAGATTGGGGCATTTGTGCCAGGA	463		
Db 181	TGAGAAATGTCAGAGCCACAGCGGCTCTTCAAGATTGGGGCATTTGTGCCAGGA	240		
Query 464	GATGGCCAAAGAGGAGTACAGACACTGGTGTCTCTCAGGGGGTAATGCGGGATGCG	523		
Db 241	GATGGCCAAAGAGGAGTACAGACACTGGTGTCTCTCAGGGGGTAATGCGGGATGCG	300		
Query 524	TGCTGCTTAATGCTGCTAGAGAACTGGGGCATTCCTGCCACATCTGTGCTCCCGAAGCAC	583		
Db 301	TGCTGCTTAATGCTGCTAGAGAACTGGGGCATTCCTGCCACATCTGTGCTCCCGAAGCAC	360		
Query 584	CTCCCTGAGAGGTGTGAGAGAGGCTCAGAGGGGAGGGGGCCAGAGTTCAGCTACGTGAGAA	643		
Db 361	CTCCCTGAGAGGTGTGAGAGAGGCTCAGAGGGGAGGGGGCCAGAGTTCAGCTACGTGAGAA	420		
Query 644	GGTCTGGAGCAGAGCCAACTTGAGGGGCGCAAGATTGGCCAAAGAGGAGAGCGCTGGAGAA	703		
Db 421	GGTCTGGAGCAGAGCCAACTTGAGGGGCGCAAGATTGGCCAAAGAGGAGAGCGCTGGAGAA	480		
Query 704	TGTCCCGCCGTTTGACACCCCTTAATATGAAAGGCCACAGCTCAGCTGTGTGACAGAGCT	763		
Db 481	TGTCCCGCCGTTTGACACCCCTTAATATGAAAGGCCACAGCTCAGCTGTGTGACAGAGCT	540		
Query 764	GAAACACTGTGTGAGAGACCCACACAGGTGCTCTGTGTGAGCAGTGTGGGGGTGGGGGCT	823		
Db 541	GAAACACTGTGTGAGAGACCCACACAGGTGCTCTGTGTGAGCAGTGTGGGGGTGGGGGCT	600		
Query 824	CCTGGCCGGGGGTGTGTGCTGGCTGGCTGTGAGAGTGG	858		
Db 601	CCTGGCCGGGGGTGTGTGCTGGCTGGCTGTGAGAGTGG	634		

RESULT 14

LOCUS BGI69688

DEFINITION 602324674F1 NIH_MGC_89 Homo sapiens CDNA clone IMAGE:447450 5'

ACCESION BGI69688

/lab_host="PH10B(phage-resistant)"

/note="Organ: kidney; Vector: pOTB1; Site.1: XhoI; Site.2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCCAGCAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."

REFERENCE 1 (bases 1 to 964)
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
<http://image.llnl.gov>
 Plate: LMNL0176 row: d column: 19
 High quality sequence stop: 716.

FEATURES
 Source
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4427490"
 /clone_lib="NIH MGC 89"
 /tissue_type="hypernephroma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: kidney; Vector: PCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."

BASE COUNT
 210 a 233 c 360 g 161 t

ORIGIN

Query Match 39.5%; Score 587.2; DB: 10; Length 964;
 Best Local Similarity 95.6%; Pred. No. 7.3e-123;
 Matches 658; Conservative 0; Mismatches 23; Indels 7; Gaps 5;

221 GGAGGCGAGGAGCTGGGCGCAGCGCTGCTGGATGTTGGAGAGGCTGTCTACT 280
 1 GGAGGCGAGGAGCTGGGCGCAGCGCTGCTGGATGTTGGAGAGGCTGTCTACT 59
 281 GGTCTCCAGATGAGCGGCGCTGTGGCAGAGCAGTCCAAAGCAGAGCGCTTACGCTGT 340
 60 GGTCTCCAGATGAGCGGCGCTGTGGCAGAGCAGTCCAAAGCAGAGCGCTTACGCTGT 119
 341 CACACCTCTGTGGAGAGCTGGGCGCTGTCCAGAGTGGCGGCGATGCTTCTCTCAA 400
 120 CACACCTCTGTGGAGAGCTGGGCGCTGTCCAGAGTGGCGGCGATGCTTCTCTCAA 179
 401 GTGTGAGATGTGACAGCGCGCTCTTCAAGATGGGGCATTTGGCATTTCTGCCA 460
 180 GTGTGAGATGTGACAGCGCGCTCTTCAAGATGGGGCATTTGGCATTTCTGCCA 239
 461 GGAGATGGCCAAAGAGGATGACACACCTGGTGTCTCTCAGAGGGGTAATGCGGGCAT 520
 240 GGAGATGGCCAAAGAGGATGACACACCTGGTGTCTCTCAGAGGGGTAATGCGGGCAT 299
 521 CGCTCTCTCTATGCTGTAGGAAGCTGGCATTCCTGCGACATGCTGCTCCCGGAGAG 580
 300 CGCTCTCTCTATGCTGTAGGAAGCTGGCATTCCTGCGACATGCTGCTCCCGGAGAG 359
 581 CACCTCTCTGAGTGTGACAGAGCTGACAGGGGAGGGGGCGAGGTTGACATGCTGAG 640
 360 CACCTCTCTGAGTGTGACAGAGCTGACAGGGGAGGGGGCGAGGTTGACATGCTGAG 419
 641 AAAGCTGTGAGCAGAGCGCAATCTGAGGGCGCAAGAGTTGGCCAGAGGAGCGCTGGA 700
 420 AAAGCTGTGAGCAGAGCGCAATCTGAGGGCGCAAGAGTTGGCCAGAGGAGCGCTGGA 479
 701 GAATGTCCCGCGTTGACACCGCCCTAATATGAAAGGCCAGCGCAGCTGTGTCAGAGA 760
 480 GAATGTCCCGCGTTGACACCGCCCTAATATGAAAGGCCAGCGCAGCTGTGTCAGAGA 539

QY 761 GCTGAAGCAGTGTGAGAGACCCACAGAGTCCCTGTGCTGCGAGTGGGGTGGGG 820
 DB 540 GCTGAAGCAGTGTGAGAGACCCACAGAGTCCCTGTGCTGCGAGTGGGGTGGGG 598
 QY 821 TCTCTGCGCGGGGTGTGCTGCTGCTGAGAGTGGGCTGGACATGTACCATAT 880
 DB 599 TCTCTGCGCGGGGTGTGCTGCTGCTGAGAGTGGGCTGGACATGTACCATATCA 653
 QY 881 TGCCATGAGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 908
 DB 654 TGCCATGAGACCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 681

RESULT 15
 AA573827/c
 LOCUS
 DEFINITION
 614 bp mRNA linear EST:1012877-3
 Similar to SW:SDHL_RAT P09367 L-SERINE DEHYDRATASE ;, mRNA
 sequence.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 614)
 NCI-CCAP <http://www.ncbi.nlm.nih.gov/nciccap>.
 AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 TITLE Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapds-remail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Stratagene, Inc., David B. Krizman, Ph.D.

CDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CCAP clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at:
www.bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1319 Std Error: 0.00
 Seg primer: -40m13 fwd. Er from Amersham
 High quality sequence stop: 445.

FEATURES
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BASE COUNT
 126 a 185 c 179 g 124 t

Query Match 39.3%; Score 583.6; DB: 9; Length 614;
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 Matches 610; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

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 QY 1461 AACACTTCTGATTTGAA 1478
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Search completed: June 5, 2002, 00:42:48
 Job time: 1836 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: June 5, 2002, 00:15:38 ; Search time 215.47 Seconds

(without alignments)
11832.821 Million cell updates/sec

Title: US-09-088-435-2

Perfect score: 1485

Sequence: 1 GGGTCGACCAACGTCGATG.....TTTCTGATTTGAAAAAAA 1485

Scoring table:

IDENTITY_NIC
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	1485	100.0	1485	22	AA512098
2	1320	88.9	1364	22	AA541108
3	1315	87.6	1396	22	AA541634
4	1303.4	87.8	1379	22	AA517992
5	1284.6	86.5	1304	22	AA159778
6	1283	86.4	1327	24	ABA02877
7	986.8	66.5	990	24	ABA02878
8	374	25.2	390	20	AA541006
9	211.4	14.2	213	15	AA057448

10	102	6.9	443	22	AA192045
11	69.2	4.7	1545	19	AAV05037
12	69.2	4.7	1545	19	AAV05038
13	69.2	4.7	1545	19	AAV05039
14	69.2	4.7	1545	20	AA24936
15	69.2	4.7	1545	20	AA24937
16	69.2	4.7	1545	20	AA24938
17	69.2	4.7	1545	20	AA24939
18	69.2	4.7	1545	20	AA24940
19	69.2	4.7	1545	20	AA24941
20	69.2	4.7	1545	20	AA24942
21	69.2	4.7	1545	20	AA24943
22	69.2	4.7	1545	20	AA24944
23	69.2	4.7	1545	20	AA24945
24	69.2	4.7	1545	20	AA24946
25	69.2	4.7	1545	20	AA24947
26	69.2	4.7	1545	20	AA24948
27	69.2	4.7	1545	20	AA24949
28	69.2	4.7	1545	20	AA24950
29	69.2	4.7	1545	20	AA24951
30	65.4	4.4	1189	23	ABL18395
31	65.4	4.4	1447	23	ABL18395
32	59.2	4.0	4403765	22	ABL18395
33	59.2	4.0	4411529	22	ABL18395
34	56.6	3.8	9243	21	AA51534
35	56.6	3.8	349980	21	AA51534
36	56.6	3.8	58909	22	AA51534
37	54.6	3.7	534720	19	AAV30458
38	54.6	3.7	536165	19	AAV30459
39	53.6	3.6	1509	20	AA21199
40	53.6	3.6	1509	20	AA21200
41	53.6	3.6	1599	20	AA21201
42	53.6	3.6	1599	20	AA21202
43	53.6	3.6	1620	20	AA21203
44	53.6	3.6	1620	20	AA21204
45	53.6	3.6	1638	20	AA21205

ALIGNMENTS

RESULT 1
AA512098 standard; DNA: 1485 BP.

AC AA512098;

DT 21-NOV-2001 (first entry)

DE Human serine dehydratase homologue (SDHH) DNA.

XX Serine dehydratase homologue; SDHH; human; cytosolic; antidiabetic; ds;
XX antithyroid; antilipemic; anorectic; noctropic; dermatological; cancer;
XX hepatocytic; metabolic; Addison's disease; cystic fibrosis; diabetes;
XX fatty hepatocirrhosis; galactosaemia; hyperadrenism; hypoadrenism;
XX hypoparathyroidism; hyperparathyroidism; hypercholesterolemia; goitre;
XX hyperthyroidism; hypothyroidism; hyperlipidaemia; hyperlipaemia; breast;
XX lipid myopathy; obesity; lipodystrophy; phenylketonuria; renal failure;
XX adenocarcinoma; leukaemia; lymphoma; melanoma; adrenal gland; bladder;
XX bone marrow; brain; cervix; heart; kidney; liver; muscle; ovary;
XX penis; prostate; pancreas; skin; spleen; testis; thymus; thyroid; uterus.

OS Homo sapiens.

XX Key Location/Qualifiers

XX CDS

291..1280

/*tag= a
/product= "Human serine dehydratase homologue"
/transl_except= (pos:885..896, aa:Met-His)
/transl_except= (pos:1125..1136, aa:Ala-Ala)

XX US6277619-B1.

PD 21-AUG-2001.
XX
EF 01-JUN-1998; 9805-0088435.
XX
ER 01-JUN-1998; 9805-0088435.
XX
PA (INCY-) INCYTE GENOMICS INC.
XX
PI Lal P, Corley NC, Guegler KJ, Patterson C;
XX
DR WPI: 2001-55133/59.
XX
P-PSDB: AAU07604.
XX
PT New human serine dehydratase homologue polypeptide, useful for diagnosis,
XX prevention and treatment of disorders of metabolism such as diabetes,
PT cystic fibrosis, obesity and cancer
XX
PS Example 5; Column 41-42; 22pp; English.

CC The sequence represents DNA encoding a human serine dehydratase homologue
CC (SDHt) polypeptide. SDHt, its fragments or its derivatives are useful for
CC treating or preventing a disorder of metabolism such as Addison's
CC disease, cystic fibrosis, diabetes, fatty hepatocirrhosis, galactosaemia,
CC goitre, hyper and hypoadrenalism, hyper and hypoparathyroidism,
CC hypercholesterolaemia, hyper and hypothyroidism, hyperlipidaemia,
CC hyperlipoproteinaemia, lipid myopathies, obesity, lipodystrophias,
CC phenylketonuria and renal failure, cancer, including adenocarcinoma,
CC leukaemia, lymphoma, melanoma and cancers of the adrenal gland, bladder,
CC bone, bone marrow, brain, breast, cervix, heart, kidney, liver, muscle,
CC ovary, penis, prostate, pancreas, skin, spleen, testis, thymus, thyroid
CC and uterus.

Query Match	100.0%	Score 1485;	DB 22;	Length 1485;
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Matches 1485; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0

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61	cggatgagggtgtgctccatccctctctctcgcgtcttccaccggaggcttagtgctg	120
121	GACCTTCTCTTAAACAAGAGAGAGACCAAGGTTCCCGAAGCTGCGTAAGCGGA	180
121	gagcttctctttaaacaaggaggaggaaccaaggttgcggaaagctgctctgaagcttga	180
181	CAGAAGCGGTCTGTGAAAGAGCTGTTCCTGGCAGGCTTGAAGGCAAGAGCTGGGGCC	240
181	cagaagcgggtcttcgtgaaagagcttgctcttccttcgcagcgttgaaaggagagcttggggcc	240
241	ACGCTGCTGTGGANATGTTGGGCAAGGAGGCTGTCTACTGTGTCCTCAGAAATGACGGCC	300
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361	gggcgctgtcccaagatggcgggacatgctgtcttctcccaagcttggaaatgtgcagccca	420
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481	GGAGACACTGTGTGTCTCTCAGGGGGTAATCGGGGCATCGGTGCTATGCTAGTGTCTA	540

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QY	1381	ctgtgcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt	1440
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XX	AA541108:		
XX			

RESULT	2
AS41108	
ID	AS41108 standard; cDNA; 1364 BP
XX	
AC	AS41108;
XX	

DT 17-DEC-2001 (first entry)
XX cDNA encoding novel human enzyme polypeptide #324.
XX
KW Human: oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW lysase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotoxic; anticoagulant; ss.
XX
OS Homo sapiens.
XX
PN WC20015301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
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PR 07-JUN-2000; 2000US-0209467.
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PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

DT 17-DEC-2001 (first entry):
XX
DE cDNA encoding novel human enzyme polypeptide #850.
XX
KW Human: oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
KW lyase; hyperproliferative disorder; immunodeficiency disorder;
KW autoimmune disorder; neurological disorder; metabolic disorder;
KW inflammatory disorder; cardiovascular disorder; reproductive disorder;
KW blood-related disorder; infectious disorder; gene therapy; cytostatic;
KW anti arthritic; nephrotoxic; anticoagulant; ss.
XX
OS Homo sapiens.
XX
PN W020015301-A2.
XX
PD 02-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01239.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180638.
PR 02-MAR-2000; 2000US-0184666.
PR 16-MAR-2000; 2000US-0186350.
PR 17-MAR-2000; 2000US-0198076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.

PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234224.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234999.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
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PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246522.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.

PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251869.
PR 11-DEC-2000; 2000US-0251990.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
DR WPI, 2001-465566/50.
XX
DR P-PSDB; AAU23764.
XX
PT Novel polypeptides and polynucleotides useful for diagnosing,
PT preventing, treating neural, immune system, muscular, reproductive,
PT pulmonary, cardiovascular, renal, proliferative disorders and cancerous
XX diseases
XX
PS Claim 4; SEQ ID NO 860; 1180bp; English.
XX
CC The present invention relates to the isolation of novel human enzyme
CC polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences
CC encoding them. The enzyme polypeptides of the invention may comprise the
CC functional classes of oxidoreductases, transferases, hydrolases, lyases,
CC isomerases or ligases. The sequences of the invention are useful in the
CC diagnosis, treatment, prevention and/or prognosis of a wide range of
CC disorders including hyperproliferative disorders (e.g. cancer),
CC immunodeficiency disorders (e.g. AIDS), autoimmune disorders
CC (e.g. arthritis), neurological disorders (e.g. Alzheimer's disease),
CC metabolic disorders (e.g. phenylketonuria), inflammatory disorders
CC (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis),
CC blood-related disorders (e.g. haemophilia), reproductive disorders
CC (e.g. infertility) and infectious disorders (e.g. influenza). The
CC polynucleotides of the invention can also be used in gene therapy.
CC AAU40785-AAU41684 represent cDNA sequences encoding for the novel human
CC enzyme polypeptides of the invention.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 1396 BP; 276 A; 380 C; 471 G; 267 T; 2 other:
SQ

Query Match 88.6%; Score 1315; DB 22; Length 1396;
Best Local Similarity 99.8%; Pred. No. 5, 6e-310;
Matches 1326; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 158 GCCGGAAGCTGCTG-AAGCTGACAGAGCCGCTTCTGGAAGAGCTGCTCCCTGCA 216
DB 39 gccggaagctgctgaagctgacagagccgcttctggaagagctgctccctgca 98
QY 217 GCGTGGAGGCGAGAGCTGGGCGACAGCTGCTGCTGGATGTTGGCGAGAGCTGCT 276
DB 99 ggcctggaagagagagagctggaagagctgctgctggaagagctgctccctgca 98
QY 277 ACCTGCTTCACAGATGAGAGGCGCTTGGCGAGAGCTGCAAGAGAGAGCCCTTACG 336
DB 159 acctgcttcacagatgagagcgcttggcgagagctgcaagagagagcccttcaag 218
QY 337 TGGTACACCTCTGTTGAGAGAGCTGGGCGCTGCTCCAGAGTGGCGGAGCTGCTTCC 396
DB 219 tggtaacacctctgttgaagagctggcgctgctccagctggcgagctgcttctcc 278
QY 397 TCAGCTGTGAGATGTGAGCGCCAGCGCTCTTCAGATTCGGGCAATTGGCATTTCT 456
DB 279 tcaagctgtgagatgtgagcgccagcgctcttcaagattcgggagcttctc 338
QY 457 GCCAGGATGCGCCAGAGGAGTGCACACACTGTGTGCTCTCAGGGGATTAATGCG 516
|||||

DB 339 gccagagatgcccagaagagatgacagactggtgtctctcctaagggttaatgcg 398
QY 517 GCATCGCTGCTGCTATGCTAGAGAGCTGGCATTCCTGGCACCATCGCTCCCG 576
DB 399 gcatcgctgctgctatgctagagagcttctccacacacgctcccg 458
QY 577 AGACACCTCCCTGCAAGAGTGTGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 636
DB 459 agacacctccctgcaagagtgagagctgcaagagagagagagagagagagagagag 518
QY 637 CTGGAAGAGTCTGGAGAGAGCCATCTGAGGCGGCAAGAGTGGCGAGAGGAGGCT 696
DB 519 ctggaagagctgagagagagagagagagagagagagagagagagagagagagag 578
QY 697 GGGAGATGTCCTCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 756
DB 579 gggagatgctccctgagagagagagagagagagagagagagagagagagagagag 638
QY 757 AGAGCTGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 816
DB 639 agagctgaaagagagagagagagagagagagagagagagagagagagagagag 698
QY 817 GGGTCTCTGCGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 876
DB 699 gggctctctgagagagagagagagagagagagagagagagagagagagagagag 758
QY 877 TCATTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 936
DB 759 taattgctgagagagagagagagagagagagagagagagagagagagagagagag 818
QY 937 TGTGACACTTCCACATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 996
DB 819 tgtgacaccttccacatcagagagagagagagagagagagagagagagagagagag 878
QY 997 CTCGGCCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
DB 879 ctccggccctgagagagagagagagagagagagagagagagagagagagagagag 938
QY 1057 AGCGTGTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1116
DB 939 agcggtgtagagagagagagagagagagagagagagagagagagagagagagag 998
QY 1117 GTGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1176
DB 999 gtgggagagagagagagagagagagagagagagagagagagagagagagagag 1058
QY 1177 GCGTGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1236
DB 1059 ggcgtggcgagagagagagagagagagagagagagagagagagagagagagagag 1118
QY 1237 GCCGAGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1296
DB 1119 gccgagagctgagagagagagagagagagagagagagagagagagagagagagag 1178
QY 1297 CCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1356
DB 1179 cccaagagagagagagagagagagagagagagagagagagagagagagagagag 1238
QY 1357 TGGCAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1416
DB 1239 tggcagatgagagagagagagagagagagagagagagagagagagagagagagag 1298
QY 1417 CTCCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1476
DB 1299 ctcttgagagagagagagagagagagagagagagagagagagagagagagagag 1358
QY 1477 AAAAAAAA 1485
DB 1359 agaaaaaa 1367
RESULT 4
AA157992

ID AA157992 standard; cDNA; 1379 BP.
 XX
 AC AA157992;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polynucleotide SEQ ID NO 195.
 XX
 KW Human; nootropic; immunosuppressant; cyostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokine; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.
 KW
 XX Homo sapiens.
 OS
 XX MO20015312-A1.
 PN
 XX 26-JUL-2001.
 PD
 XX 26-DEC-2000; 2000WO-US34263.
 PF
 XX 21-JAN-2000; 2000US-0488725.
 PR
 XX 25-APR-2000; 2000US-0552317.
 PR
 XX 09-JUL-2000; 2000US-0598042.
 PR
 XX 19-JUL-2000; 2000US-0620312.
 PR
 XX 03-AUG-2000; 2000US-0653450.
 PR
 XX 14-SEP-2000; 2000US-0662191.
 PR
 XX 19-OCT-2000; 2000US-0693036.
 PR
 XX 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR MPI: 2001-442253/47.
 DR P-PSDB: AAM38836.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Claim 1; SEQ ID NO 195; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM4213) with nootropic,
 CC immunosuppressant and cyostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localised neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
 CC assays for receptor activity, arthritis and inflammation, Leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 CC Sequence 1379 BP; 264 A; 382 C; 468 G; 265 T; 0 other;
 SO

Query Match 87.8%; Score 1303.4; DB 22; Length 1379;
 Best Local Similarity 99.9%; Pred. No. 3,76-307;
 Matches 1304; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 181 CAGAGCCGCTTCGGAAGAGCTGCTCCCTGCAGAGCTGAGGAGAGAGCTGGGCCC 240
 DB 72 cagagccgcttcctggaagagctgctccctgcagagctgagagagagagagagagagc 131

QY 241 ACGCTGCTCGGATGATGTTGGGAGGAGGCTGTACTGCTTCAGAAATGAGAGGCC 300
 DB aagctgctcgtggaagagctggaagagagagagagagagagagagagagagagagagc 191
 QY 301 CTGTGGCAGAGCATGCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
 DB ctgtgagagagagagagagagagagagagagagagagagagagagagagagagagag 251
 QY 361 GGGGCTGTCCAGAGTGGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
 DB 252 ggggctgtccagagagagagagagagagagagagagagagagagagagagagagagc 311
 QY 421 GCGGCTCTTCAAGATGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
 DB 312 gcggtctctcaagagagagagagagagagagagagagagagagagagagagagagat 371
 QY 481 GCAGACACCTGCTGCTCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
 DB 372 gcagacacctgtgtgtctctcagagagagagagagagagagagagagagagagagc 431
 QY 541 GGAAGCTGGGATTCCTGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
 DB 432 ggaagctgggattcctcagagagagagagagagagagagagagagagagagagagc 491
 QY 601 AGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
 DB 492 agagctgagagagagagagagagagagagagagagagagagagagagagagagagc 551
 QY 661 ATCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
 DB 552 atctgagagagagagagagagagagagagagagagagagagagagagagagagagc 611
 QY 721 ACCCTTATATGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
 DB 612 acccttataatgaaagagagagagagagagagagagagagagagagagagagagc 671
 QY 781 CCCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
 DB 672 cccacagagagagagagagagagagagagagagagagagagagagagagagagagc 731
 QY 841 CTGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 900
 DB 732 ctggctctgagagagagagagagagagagagagagagagagagagagagagagagc 791
 QY 901 CACACTGCTTAATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
 DB 792 cacactgcttaatgagagagagagagagagagagagagagagagagagagagagagc 851
 QY 961 GTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
 DB 852 gtgtgagagagagagagagagagagagagagagagagagagagagagagagagc 911
 QY 1021 TGTGCAAGATTCATCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
 DB 912 tgtgcaagattcatctgagagagagagagagagagagagagagagagagagagagc 971
 QY 1081 TCTGTGATGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
 DB 972 tctgtgatgatgagagagagagagagagagagagagagagagagagagagagagc 1031
 QY 1141 ACTGAGGCTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1200
 DB 1032 actgagacctctgagagagagagagagagagagagagagagagagagagagagagc 1091
 QY 1201 TTGTGATATGCTGTGTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1260
 DB 1092 ttgtgatattgtgtgtgagagagagagagagagagagagagagagagagagagagc 1151
 QY 1261 CCCAGCTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1320
 DB 1152 cccagctgggagagagagagagagagagagagagagagagagagagagagagagagc 1211

	inucle	gaps	0
195 GGAAAGACCTCCCTTCCCCCAGGCGGGG			

Dd	11	ggaatcgcgtgcttccctcctgcaagcctgagagcagctgagccacgcctgcttggga	2
Qy	255	TAGTTGGGCGAGGAGGCGTGTACTCTGTGTCCAGAAATGAGCGCCCTGTGGCAGCAT	31
Dd	71	taattgagcagagagcgctgctaactgcttccaaagaaagagccctgtgcaagagcat	133
Qy	315	GCCAAGCGAGGAGCCCTTTACGTGTGCACACCTCTGTTGGAGAGCTGGGCGCTGCCAG	374
Dd	131	gccaaagcagagcccttccacgtgctcaacccttgcttgagagctgagcgtlcccaag	190
Qy	375	GTGGGGGCGATGCGCTGTCTTCTCAAGTGTGAATGTGCACCACCGCGCTCTTCAAG	434
Dd	191	gtggcgggcatgctgcttcttcccaagctgagaaatgtgcagcccaagcgctccttaag	250
Qy	435	ATTGGGGGCAATGGGCATTTTCTGCCAGAGATGGCCAAAGAGGAGTGCAGACCTGGTG	494
Dd	251	atccggggcatttggcattcttgcagagagatgycgaagaggaatgcagaacctggtg	310
Qy	495	TGCTCTCAGGGGGTAAATCGGGCAATCGGTGCTGTGCTATGCTACGAAAGCTGGCAAT	554
Dd	311	tgctccctcaggggtaatgctgagcatgcgtgcctcctgctcctaagctgaagcctggcatt	370
Qy	555	CTGCGCACCATCTGTGCTCCCGCAGAGACACTCTCCGTGCAGAGTGTGCAGAGGCTGCAGGG	614
Dd	371	cctgcacacatcgtgctcccccgaagacacctccttgaagctgtgtgcagagctgcagggg	430
Qy	615	GAGGGGCGGAGGTTCACTGATGATCGGAAGGCTCTGGAGACAGGCGCAATCGAGGGGCA	674
Dd	431	gagggggccgaagttctcaactgactgagaaagttctgggacgaagccaatctgagggcgcaa	490
Qy	675	GAAATTGGCCAAAGAGGAGCGGCGGGAAGATGTCCCGCTTTACCAACCCCTAATATGG	734
Dd	491	gaattggccaaagagagacgctgaggaagaaatgctcccccgtttgacacacccctaataatg	550
Qy	735	AAAGCGCACCGCAGCTGTGTGCACGAGACTTAAAGCAATGTGTGAGCAACCCACAGTACC	794
Dd	551	aaaggccacgcacagcctgtgtgcagagctgaagacagctgtgaggaacccacacaggtgccc	610
Qy	795	CTGGGCTGGGCAAGTTGGGGGGGGGGGCTCTCTGGCGCGGGGTGTGGCTGGCTGTGGAG	854
Dd	611	ctggctgtgcagctgtgggggtgtctctcctgcggcgggggtggtgtgcctgtcctgag	670
Qy	855	GTGGGCTGGGCAATGTACCATCATATTGCCATGAGACCCATGGGGGCACTGCTTCAAT	914
Dd	671	gtgggctgggcagcctgaaccatcatctgcacatgagacccatgggggcacactgttcaat	730
Qy	915	GCGGCCATCACAGCGCGCAGGCTGTGCACACTTCCAGACATCACAGGTGTGGCCAGAGCG	974
Dd	731	gcggccatcacagccgycgaagctgtgtcacacttccagacatccaccaggtgtgcacaagag	790
Qy	975	CTGGGTCACCAAGACGGGGCGCGCTGTGGGCGCTTGGAGTGCATGACAGGTTGCAGATTAC	1034
Dd	791	ctgggtgtccaaagccggtgtgcgctgcggccctgtgagctgacgtgcaggtgtgcaaatccac	850
Qy	1035	TCTGAATGCTGGAGGACACCGAGGCTGTGACCGCTGTGCAGCAGCTCTGGATGTATGAG	1094
Dd	851	tctgaatgtgtgagagacacacgaagcctgtgagcgtgtgtgcagcagctccctcgatctgag	910
Qy	1095	CGTATGCTGGTGAGCTCTCTGTGGGCGACCTTTAGACGACATCTTACTACGAGCCTCTGG	1154

RESULT	5	
ID	AA159778	
XX	AA159778	Standard; CDNA; 1304 BP.
AC	AA159778;	
XX		
DT	22-OCT-2001	(first entry)
XX		
DE	Human polynucleotide SEQ ID NO 3767.	
XX		
KW	Human; nocotropic; immunosuppressant; cytosolic; gene therapy; cancer;	
KW	peripheral nervous system; neuropathy; central nervous system; CNS;	
KW	Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;	
KW	amyotrophic lateral sclerosis; Shy-Drager syndrome; chemotactic;	
KW	chemokine; thrombolytic; drug screening; arthritis; inflammation;	
KW	leukaemia; ss.	
XX		
OS	Homo sapiens.	
XX		
PN	MO20015312-A1.	
XX		
PD	26-JUL-2001.	
XX		
PF	26-DEC-2000; 2000WO-US34263.	
PR	21-JAN-2000; 2000US-0488725.	
PR	25-APR-2000; 2000US-0552317.	
PR	09-JUL-2000; 2000US-0598042.	
PR	19-JUL-2000; 2000US-0620312.	
PR	03-AUG-2000; 2000US-063450.	
PR	14-SEP-2000; 2000US-0662191.	
PR	19-OCT-2000; 2000US-0693036.	
PR	29-NOV-2000; 2000US-0727344.	
XX		
PA	(HYSE-) HYSEQ INC.	
XX		
PI	Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;	
PI	Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;	
PI	Zhao Q, Zhou P, Goodrich R, Dirmnac R;	
XX		
IDR	WPI: 2001-442253/47.	
XX	P-PsDB; AA040622.	
XX		
PT	Novel nucleic acids and polypeptides, useful for treating disorders	
PT	such as central nervous system injuries -	
XX		
PS	Claim 1; SEQ ID NO 3767; 10078pp; English.	
XX		
CC	The invention relates to human nucleic acids (AA157798-AA161369) and	
CC	the encoded polypeptides (AA038642-AA042213) with nocotropic;	
CC	immunosuppressant and cytosolic activity. The polynucleotides are useful	
CC	in gene therapy. A composition containing a polypeptide or polynucleotide	
CC	of the invention may be used to treat diseases of the peripheral nervous	
CC	system, such as peripheral nervous injuries, peripheral neuropathy and	
CC	Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic	
CC	lateral sclerosis, and Shy-Drager Syndrome. Other uses include the	
CC	utilisation of the activities such as: immune system suppression,	
CC	Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic	
CC	and thrombolytic activity, cancer diagnosis and therapy, drug screening,	

Claim 1; SEQ ID NO. 3767; 10078bp; English.

such as central nervous system injuries - for treating disorders

P-PSDB; AAM40622.

Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Zhao QA, Zhou P, Goodrich R, Dimanac RT, Qian XB, Ren F, Wang D, Yang Y, Zhang J

(HYSE-) HYSEQ INC

49 NOV - 2000; 200000

14-SEP-2000; 2000
19-OCT-2000; 2000

03-AUG-2000; 2000

09-JUL-2000; 2000

21-JAN-2000; 2000

26-DEC-2000; 2000

20 JUL 2001

MOZ00103312-AL.

1. **THEORY**

100

chemokine; the leukocyte

Alzheimer's; Parkinson's; amyotrophic lateral sclerosis

peripheral nervous system, oculomotoric,

0

Discussion

22-OCT-2001 14:41

AAI59778:

AAI59778 standar

SULT 5

1332 +000000000000+

1441 TCCGACCAACTC

1272 ctgtgcaactg

1381 CTGTGCACTG

1212 ggacagtcctg

1321 GGACAGTCCTC

Thu Jun 6 11

Db 911 cgtatcgtgtgagcctccctggtgagccttagcagcattactcagcctctg 970
 QY 1155 GCGAGGCTCCAGCGAGGCGCTGCGCCCTTCCCTACTCACTGTTGTAATCGTG 1214
 Db 971 cggagagctccagcggagcgtcgtccctccctcctgactcagttgtgtaatcgtg 1030
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 Db 1031 tctgtaggcaacaacatcacacgcgcgagagcgtcgcaggtcttgaataaccactggcgag 1090
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 Db 1091 gctctgaggggtcccatccctgcgcgaagaacccctgagagcgcctgacgtcctggt 1150
 QY 1335 CTGGATGAGGAGGAGCTGCTGTCAGATGAGTGAAGAGTGGCCCTGCACTGCTGTC 1394
 Db 1151 cctgagtaggagagcctcagctgagcagatgagcagtggaagctgcctgtgcaactgtgc 1210
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 Db 1211 tggcagctccctgaaagagcctcctgagctcttcttcttggcctccgacaactcgg 1270
 QY 1455 CCAATTAACACTTCTGTAATTAATAAAAAA 1485
 Db 1271 ccaataaacacttctgtaattgagaaaaa 1301

RESULT 6

ABA02877 standard; CDNA: 1327 BP.

ABA02877; 14-FEB-2002 (first entry)

Human DHY encoding cDNA SEQ ID NO 1.

Human; DHY; serine/threonine dehydratase; cytosolic; neuroprotective;
 neurotropic; antiparkinsonian; anticonvulsant; tranquilizer;
 cerebroprotective; hypotensive; antianemic; antianginal; antidepressant;
 anorectic; antimigraine; antiarteriosclerotic; vasodilator; vulnerary;
 cardiulant; antiarrhythmic; cellular proliferation; growth;
 differentiation; cell migration; metabolism; catabolism; cell signalling;
 growth factor; cytokine; Alzheimer's disease; Parkinson's disease;
 Huntington's disease; multiple sclerosis; obesity;
 ischaemia reperfusion injury; ss.

Homo sapiens.

Key Location/Qualifiers

CDS 107..1096
 /tag=a
 /product="DHY"

W0200181559-A2.

01-NOV-2001.

25-APR-2001; 2001WO-USA0609.

26-APR-2000; 2000US-199801P.

(MILL-) MILLENNIUM PHARM INC.

Meyers R;

WPI: 2002-034443/04.

P-PSDB; AAM52238.

Novel human serine/threonine dehydratase polypeptide and nucleic acid molecules for diagnosing, treating cell proliferative, neurodegenerative, musculoskeletal, cardiovascular disorders and

PR Identifying modulators
 XX
 PS Claim 1: Fig 1: 97pp: English.

The invention relates to an isolated human serine/threonine dehydratase (DHY) polypeptide and the encoding polynucleotide with cytosolic, neuroprotective, neurotropic, antiparkinsonian, anticonvulsant, tranquilizer, cerebroprotective, hypotensive, antianemic, antianginal, antidepressant, anorectic, antimigraine, antiarteriosclerotic, vasodilator, vulnerary, cardiulant and antiarrhythmic activity. DHY is useful as a modulating agent in regulating cellular proliferation, growth, differentiation or cell migration. DHY modulates metabolism or catabolism of biochemical molecules, intra or inter-cellular signalling and production of growth factors and cytokines and provides both prophylactic and therapeutic methods of treating a subject at risk of disorders associated with unwanted DHY expression or activity e.g. a DHY-associated disorder such as a CNS disorder, cellular proliferation, growth, differentiation or migration disorder, musculoskeletal or cardiovascular disorder. The DHY-associated disorders include CNS disorders such as cognitive and neurodegenerative disorders including Alzheimer's disease, dementias, Parkinson's, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis, epilepsy, autonomic function disorders such as hypertension and sleep disorder and neurophysiologic disorders, such as depression, schizophrenia, mania, anxiety disorders, learning or memory disorders e.g. amnesia, attention deficit disorder, obsessive-compulsive disorder, anxiety, phobias, panic disorder, bipolar affective disorder e.g. severe bipolar affective and bipolar affective neurological disorders, e.g. migraine and obesity, cardiac related disorders, including arteriosclerosis, ischaemia reperfusion injury, restenosis, angina, heart failure, coronary heart disease, arrhythmia, disorders of the musculoskeletal system such as paralysis and muscle weakness, e.g. ataxia, myotonia and myokymia. The DHY molecules are involved in signal transduction mechanisms involved in cellular growth, differentiation and migration and are useful for treating cancer, hepatic disorders and haematopoietic and/or myeloproliferative disorders, and disorders affecting tissues in which DHY protein is expressed. DHY can be used in gene therapy as a modulator of cell proliferation, differentiation and migration.

Sequence 1327 BP; 267 A; 361 C; 446 G; 253 T; 0 other:

Query Match 86.4%; Score 1283; DB 24; Length 1327;
 Best Local Similarity 99.6%; Pred. No. 3.3e-302;
 Matches 1286; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 187 CGGTCTCTGGAAGAGCTGCTTCCTGCGAGCTGAGGCGAGAGCTGGGCCACGCTG 246
 Db 3 cgcgtccggaagagcgtgttccctgagcgtgagagcagagcgtggccacgctg 62
 QY 247 GCTGGGATGAGTGGGAGGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 306
 Db 63 gctcggatagcttggcagagagcgtcctacgtgctccgaagtgcagcctcgtgg 122
 QY 307 CAGAGCATGCCAAGAGAGAGCCCTTTCAGAGTGTGACACCTCTGTTGAGAGACTGGGCGC 366
 Db 123 cagagcatgccaagcagagagccttcaacgtgtgtaacacctgtgtgagagcgtggcgc 182
 QY 367 TGTCCAGAGTGGGCGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 426
 Db 183 tgtccagagtggcggcagcgtcctgtcttccctcaagtgtggaatgtgcagccagcgcgt 242
 QY 427 CCTCAAGATTCGGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
 Db 243 cctcaaatctcgggagcagcagccttccgcaagaatgagcagaagaggaatgcaaac 302
 QY 487 ACCTGCTGCTCTCAGAGGAGGTAATGCGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 546
 Db 303 accgtgtgtgtcctccaggggtgtaatgagcagcagcgtcgtcgtcgtcgtcgtcgtcgtcgt 362
 QY 547 TGGGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 606
 Db 363 tgggattctcgtccacacatgctcctcccgagagactcctgcaaggtgtgtgagagagc 422

Sequence 990 BP; 185 A; 276 C; 343 G; 186 T; 0 other;

Query Match 66.5%; Score 986.8; DB:24; Length 990;
Best Local Similarity 99.8%; Pred. No. 3.1e-230;
Matches 988; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY 291 ATGACGCGCCCTGTGGCAGACATGCCAAGCAGAGAGCCCTTTCAGTGTGACACACTCTG 350
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Db 1 atgacgccccctgtggcagacatgcccaagcagagcccccttccacgtgtacacacctg 60
   |||||||

QY 351 TTGAGAGACTGGGCGCTCTCCAGGTGGCGGCATGCTGTCTTCTCTCACTGTGAGAT 410
   |||||||
Db 61 ttgagagctgtggcgtctccacagtgcgagcaltgctctcctcaagtgtagat 120
   |||||||

QY 411 GTGAGAGCCACGCGCTCTTCAAGATTTGGGGCATTTGGGCAATTTGTGACAGATGAGCC 470
   |||||||
Db 121 gtgacagccccgccccctcctcaagatctgggacatctgtgacatcttctgcagagatgccc 180
   |||||||

QY 471 AAGAAGGATGCAGACACTGTGTCTCTCAGGGGTAATGCGGCGCATGCTCTGCC 530
   |||||||
Db 181 aagaagagatgcagacacctgtgtgtctccacaggggtaatgcgagcatgctgtgccc 240
   |||||||

QY 531 TATGCTGTAGGAAGCTGGCGATTCTGCCACATGCTGTCTCCCGAGAGACACTCTCCTG 590
   |||||||
Db 241 tatgtctaggaagctgtgcatctctgcacacatcgtctcccgagagacacctccctg 300
   |||||||

QY 591 CAGGTGTGCAAGAGGCTCAGGGGAGGGGCGCCAGGTTCACGTACACTGAGAAAGTCTGG 650
   |||||||
Db 301 caggtgtgcagagagctgcagagcgagggcgaggttcacgtacacagagagctgcgg 360
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QY 651 GACGAGGCCAATCTGAGGGGCGCAAGAGTGGCCAAAGAGGAGCGGTGAGATGTCCCC 710
   |||||||
Db 361 gacgagggcaatctgagggcgcaagaggttgcgaagagggcgctgtggaatgtccccc 420
   |||||||

QY 711 CCGTTTGACACCCCTTAATATGGAAGGCCACGCCACCTGTGTGACAGAGCTGAAGCA 770
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Db 421 ccglttgacccccctcctaatatgtgaaagccagccagcctgtgcaagagctgaaagca 480
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QY 771 GTGCGAGAGACCCACACGAGTGGCTGTGCTGTGAGTGGGGGTGGGGGTCTCTGCGCC 830
   |||||||
Db 481 gtgcgaagagaccacacacagctgccccgtgtgtgtgcaaglttgagggtgtctcttgcgc 540
   |||||||

QY 831 GGGGTGTGCTGTGCTGTGAGGTGGGCTGGCGCATGATACCCATATTGCCATGTAGAG 890
   |||||||
Db 541 ggggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
   |||||||

QY 891 ACCCATGGGCGACACTGTCTTAATGCGGCATTCACAGCGCGCAAGCTGTGACACTTCCA 950
   |||||||
Db 601 acccatgggacacactgtctcaatgtgcacatcacagcgagcaagctgtgtcacacttcca 660
   |||||||

QY 951 GACATACACACTGTGCGCCAAAGGCTGGTGCCTGCAAGAGGTGGCGGCGGCGCTGTGAG 1010
   |||||||
Db 661 gacatcaccaatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
   |||||||

QY 1011 TGCATGACAGGTGTGCAAGATTCACCTTGAAGTGTGAGAGACACGAGGCTGTGAGCCCT 1070
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Db 721 tgcattgaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 780
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QY 1071 GTGACAGACGCTCTGTGATGATGACGATGCTGTGTGAGAGCTGTGAGGCGAGCCCTTA 1130
   |||||||
Db 781 gtgacagacgctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 840
   |||||||

QY 1131 GCAGCCATCTACTAGGCTCTCTGCGAGGCTCCAGGCGGAGGCTGCTGCCCTTCC 1190
   |||||||
Db 841 gcagccatctactaaggctctctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 900
   |||||||

QY 1191 CTGACTTCAGTGTGTGATGTGTGTGTGAGAGCAACATCACAAGCGGAGAGTGTGAG 1250
   |||||||
Db 901 ctgacttcagttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
   |||||||

QY 1251 GCTTTGAAAACCAACCTGGCGAGGTGCA 1280
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Db 961 gcttgaaccacacctgtggccaggtctga 990

```

RESULT 8
ID AAX41006 standard; CDNA: 390 BP.
XX
AC AAX41006:
XX
DT 18-JUN-1999 (first entry)
XX
DE Human secreted protein 5' EST SEQ ID NO: 218.
XX
KW Human; secreted protein; EST; expressed sequence tag; diagnosis;
KW forensic; gene therapy; chromosome mapping; signal peptide;
KW upstream regulatory sequence; cytokine activity; cell proliferation;
KW differentiation; haematopoiesis regulation; tissue growth regulation;
KW reproductive hormone regulation; chemotactic; chemokinetic; haemostatic;
KW thrombolytic; anti-inflammatory; tumour inhibition; ds.
XX
OS Homo sapiens..
XX
PN W0906554-A2.
XX
PD 11-FEB-1999.
XX
PE 31-JUL-1998; 98WO-IB01238.
XX
PR 01-AUG-1997; 97US-0905134.
XX
PA (GEST ) GENSET.
XX
PI Duclert A, Dumas Milne Edwards J, Lacroix B;
XX
DR WPI: 1999-153784/13.
XX
DR P-PSDB: AAY12173.
XX
PT New nucleic acids encoding human secreted proteins - obtained from
PT cDNA libraries prepared from kidney, fetal kidney, dystrophic
PT muscle, muscle and heart tissue
XX
PS Claim 1; Page 315-316; 622pp; English.
XX
CC AAX40826 to AAX41093 represent 5' expressed sequence tags (ESTs) for
CC human secreted proteins, and encode the proteins given in AAY01602 and
CC AAY11994 to AAY12260, respectively. The proteins given represent the
CC signal peptide and an N-terminal fragment of a secreted protein. The
CC nucleic acid sequences can be used for producing secreted human gene
CC products. They can also be used to develop products for diagnosis and
CC therapy. The proteins obtained may have cytokine activity, cell
CC proliferation/differentiation activity, haematopoiesis regulating
CC activity, tissue growth regulating activity, reproductive hormone
CC regulating activity, chemotactic/chemokinetic activity, haemostatic and
CC thrombolytic activity, receptor/ligand activity, anti-inflammatory
CC activity, tumour inhibition activity or other activities. The products
CC can be used in forensic, gene therapy and chromosome mapping procedures.
CC The sequences can also be used for obtaining corresponding promoter
CC sequences. The nucleic acids encoding of the signal peptide can be used
CC for directing extracellular secretion of a polypeptide or the insertion
CC of a polypeptide into a membrane, or importing a polypeptide into
CC a cell.
XX
SO Sequence 390 BP; 72 A; 103 C; 135 G; 79 T; 1 other;

Query Match 25.2%; Score 374; DB:20; Length 390;
Best Local Similarity 99.5%; Pred. No. 2.2e-81;
Matches 385; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

Length 213
Indels 0: Gaps 0

CC The invention relates to human polypeptides AA179941-AA193441) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity eliciting
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polypeptides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, hematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.

CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pat_sequences.
XX
XX Sequence 443 BP, 110 A; 115 C; 129 G; 89 T; 0 other;

[illegible]

KM Threonine deaminase; enzyme; transgenic plant; soybean; substrate; ds
KM Threonine deaminase; enzyme; transgenic plant; soybean; substrate; ds
KM metabolic pathway; biosynthesis; 3-hydroxybutyrate; 3-hydroxyvalerate

QY	499	CCCTAGAGGGGTAATAGCGGAGCATGCGTGTGCTCCATCTCTCTGTAGGAAGCTGGCAATTCCG	558
Db	254	ctctcgtcggttaacacaacgcgcgcgtcgtcgtcttctctctcgcgcgttaagcgtcgtgaag	313
QY	559	CCACCAATCGTGCCTCCCGAGAGCAGCACTCCCTGCAGGTGGTGCAGAGGCTCAGAGGGGAGG	618
Db	314	ccctgatacttataagcaaccgcacccgcgaatacaagtcgaccgcgttcgcgcgtcttcg	373
QY	619	GGGCGCCAGGTTCACTGACTGGAAGGCTGTGGACAGGCGCAATCTGAAGGCGCAAGACT	678
Db	374	gcgcgcgaagctgctcgtctccacgcgcgcgaactttgataaagcaaacgcgaacgcgtatcgaac	433
QY	679	TGGCGAAGAGGAGGAGCGGTGTGGAGAAATGTCOCCTGGTGAACCCCTTGAACCCCTTAATATGGAAG	738
Db	434	ttgtacagcgcgcgaaggggttcaactctgtgtgtgcgcgcgtcttcacatccgtatgtgtatctgcg	493
QY	739	GCCACGCGCACTGTGTGCACAGAGCTGAAGAAGTGTGTAAGAGACCCACACAGGTGTCCTGG	798
Db	494	ggaacaggcaacgcgtgcgtctgaactt-----ctcacgaaggaagccatctcgcacgcg	547
QY	799	TGCTGCGAGTTGGGGGGTGGGGGTTCTCTCGCGGGGGTGTGCTGTGGCTCTGAGAGGTGG	858
Db	548	tatttctgtcagtcgcgcgcgcgtctgcgtctgtctgtcgtgtgcgtctgatacaaac	607
QY	859	GCTGCGACGATGATACCCATTCATTCGATGGAGACCAACCATGGGGACACACTGCTTCATTCGGG	918
Db	608	tgatgtccgcgaatacaagaatgtatctgcgcgtctgaagcggaaagactctgcgtctcgtgaagaag	667
QY	919	CCATACACAGCGGGCAAGCTGTGCACACTTCCAGACTCACAGTGCATGGGCAAGAGCTCGG	978
Db	668	cgcctgtgactgcgcgttcatccggttgcatactcgcgcgcgcgttaaggtcatttgcctaaggcgttaag	727
QY	979	GTCGCAAGAGAGGTGGCCCTCGGGCCCTGGAGTGCATGACAGGTGTGCAAGATTCACTCTG	1038
Db	728	cgtgtaaaacgcatacgttgtaagaaacttccgtttatgcaggaagtatctcgaacgacatca	787
QY	1039	AAGTGTGGAGGACCCGAGGCTGTGAGCGCTGTGCAGCAGCTCCTGGATGATGAGCGTA	1098

Thu Jun 6 11:33:58 2002

us-09-088-435-2.rng

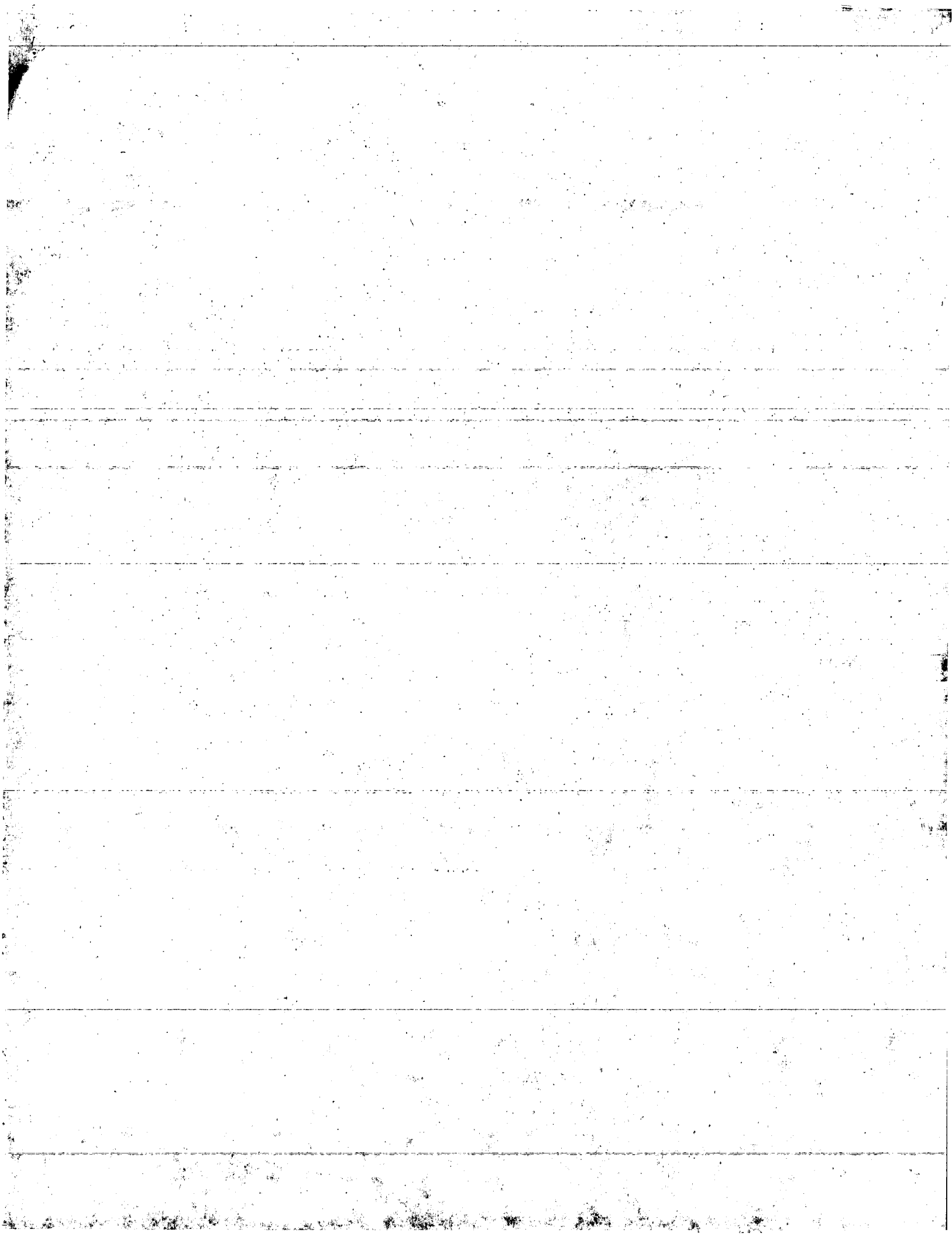
Page 17

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QY 1099 TGTGTGTGAGACCTTGCCTGTGGGAGAGCTTACAGCCAT 1138

Db 848 cgtgagcgaaccctctgagcgctgagcgtgaggaat 887

Search completed: June 5, 2002, 01:22:15
Job time: 3997 sec



QY 786 CCAAGTCCCTGCTGCTGCAATTTGGGGGTGGGGGTCTCTGCGCCGGGATGCTGGC 845
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 QY 846 CTGCTGAGAGTGGGCTGCGCAGCATGTACCATCATTTGCCATGAGAGACCATGGGACAC 905
 DB 61 CCGCTGAGAGTGGGCTGCGCAGCATGTACCATCATTTGCCATGAGAGACCATGGGACAC 120
 QY 906 TGGCTCAATGCGGCAATCAACAGCCGCAAGCTGCTACACTTCCAGACATCAACAGTGTG 965
 DB 121 TGCTCAATGCGGCAATCAACAGCCGCAAGCTGCTACACTTCCAGACATCAACAGTGTG 180
 QY 966 GCCAAGAGCTTGGGCTGCGCAGCATGTGCGGCT 998
 DB 181 GCCAAGAGCTTGGGCTGCGCAGCATGTGCGGCT 213

RESULT 10

RESULT 9

AA057448 standard; CDNA to mRNA; 213 BP.

AA057448;

19-OCT-1994 (first entry)

Ser dehydrogenase like protein.

Human CDNA; library; enzyme; protein; ss.

Homo sapiens.

17-FEB-1994.

04-AUG-1993; 93WO-JP01095.

04-AUG-1992; 92JP-0208077.

13-NOV-1992; 92JP-0327619.

26-FEB-1993; 93JP-0061431.

(SAGA) SAGAMI CHEM RES. CENTRE.

Iwahori A, Kato S, Kato T, Kim N, Oh S, Sekine S;

WPI: 1994-065688/08.

P-PSDB; AAR46109.

CDNA of human origin and proteins coded by it - which may be expressed by in vivo or in vitro translation using sense RNA or antisense DNA corresponding to the CDNA.

Claim 1; Page 68; 167pp; Japanese.

mRNA expressed in human fibrosarcoma cell line HUT-78 was

isolated and used to construct a CDNA library using vector

pTZ18Rpl. Clone HP00157 encoding Ser dehydrogenase-like protein

was isolated.

Sequence 213 BP; 34 A; 62 C; 77 G; 40 T; 0 other;

Query Match 14.2%; Score 211.4; DB 15; Best Local Similarity 99.5%; Pred. No. 6.1e-42; Matches 212; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 15
 AA573827/c
 LOCUS AA573827 614 bp mRNA linear
 DEFINITION nk08b03.s1 NCI_CGAP_Co2 Homo sapiens cDNA clone IMAGE:1012877
 similar to SW:SDHL_RAT P09367 L-SERINE DEHYDRATASE ; mRNA
 sequence.
 ACCESSION AA573827
 VERSION AA573827.1 GI:2348342
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 614)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: Stratagene, Inc., David B. Krizman,
 Ph.D.
 cDNA Library Arraying: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 1319 Std Error: 0.00
 Seq primer: -40m13 fwd. ET from Amersham
 High quality sequence stop: 445.
 FEATURES
 source Location/Qualifiers
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 /db_xref="taxon:9606"
 /clone="IMAGE:1012877"
 /clone_lib="NCI_CGAP_Co2"
 /tissue_type="tumor"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: colon; Vector: Bluescript SK-; Site_1: EcoRI
 ; Site_2: XhoI; Cloned unidirectionally. Primer: Oligo
 dT. Bulk colon villous adenoma. 5' adaptor sequence: 5'
 GAATTCGGCAGAG 3' 3' adaptor sequence: 5'
 CTCGAGTTTTTTTTTTTTTTTTTT 3' Average insert size: 1.1 kb."
 BASE COUNT 126 a 185 c 179 g 124 t
 ORIGIN

Query Match 39.3%; Score 583.6; DB.9; Length 614;
 Best Local Similarity 98.7%; Pred. No. 4.2e-122;
 Matches 610; Conservative 0; Mismatches 4; Indels 4; Gaps 2;

QY 861 TGGCAGCATGTACCCATCATTGCCATGGAGACCCATGGGGCACACTGCTTCAATGCGGCC 920
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 614 TGGCAGCATGTACCCATCATTGCCATGGAGACCCATGGGGCACACTGCTTCAATGCGGCC 555
 QY 921 ATCACAGCCGGCAAGCTGGTCCACTTCCAGACATCACCAGTGTGGCCAAGAGCCTGGGT 980
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 554 ATCACAGCCGGCAAGCTGGTCCACTTCCAGACATCACCAGTGTGGCCAAGAGCCTGGGT 495

Thu Jun 6 11:33:59 2002

us-09-088-435-2.rst

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Db	494	GCACAAAGACGGTGGCCGCTCGGGGCCCTGGAGTGCATGCATGCAGAGGTGTGCAAGATTCACTCTGAA	435
OY	1041	GTGTGTGAGAGACACCGAGAGGCTGTGAGGCTGTGAGCAGTCTGTGATATGATGAGCCATG	1100
Db	434	GTGTGTGAGAGACACCGAGAGGCTGTGAGGCTGTGAGCAGTCTGTGATATGATGAGCCATG	375
OY	1101	CTGTGTGAGAGCTGCCTGTGAGGGGACACTTATGACCATCTACTCAGGCTCTCTGCGAGG	1160
Db	374	CTGTGTGAGAGCTGCCTGTGAGGGGACACTTATGACCATCTACTCAGGCTCTCTGCGAGG	318
OY	1161	CTCCAGGCGAGGGCTGCTGCCCTTCCCTTCTGACTTTCAGTTGTGTGTATCTGTGTGA	1220
Db	317	CTCCAGGCGAGGGCTGCTGCCCTTCCCTTCTGACTTTCAGTTGTGTGTATCTGTGTGA	259
OY	1221	GGCAACAACATCAACAGCCGAGAGCTGACAGGCTTTGAAAAACCACTGGGCCAGGTCTGA	1280
Db	258	GGCAACAACATCAACAGCCGAGAGCTGACAGGCTTTGAAAAACCACTGGGCCAGGTCTGA	199
OY	1281	GGGGTCCCATCTTGCCCCCAAGACCCTTGAGAGGCCCATGAGACATGCTGATCTGGAT	1340
Db	198	GGGGTCCCATCTTGCCCCCAAGACCCTTGAGAGGCCCATGAGACATGCTGATCTGGAT	139
OY	1341	GAGGAGAGACTGAGTCTGGCAGATGGCAGTGGAACTGCGCCCTGTGCAACTGTGCTGCTG	1400
Db	138	GAGGAGAGACTGAGTCTGGCAGATGGCAGTGGAACTGCGCCCTGTGCAACTGTGCTGCTG	79
OY	1401	CGCTCTGAAGAGAGCCCTCTTGAGCTGCTTTTGGCTCTCCGACAACTCCGGCCATA	1466
Db	78	CGCTCTGAAGAGAGCCCTCTTGAGCTGCTTTTGGCTCTCCGACAACTCCGGCCATA	19
OY	1461	AACACTTCTGAATTGAA	1478
Db	18	AACACTTCTGAATTGAA	1

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